

Figure 1.

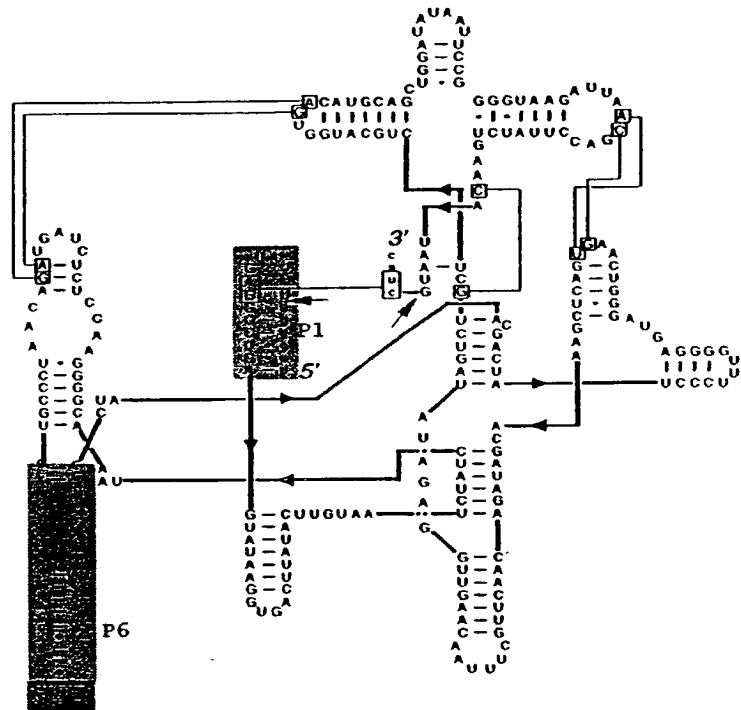
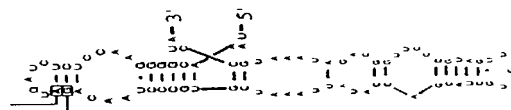
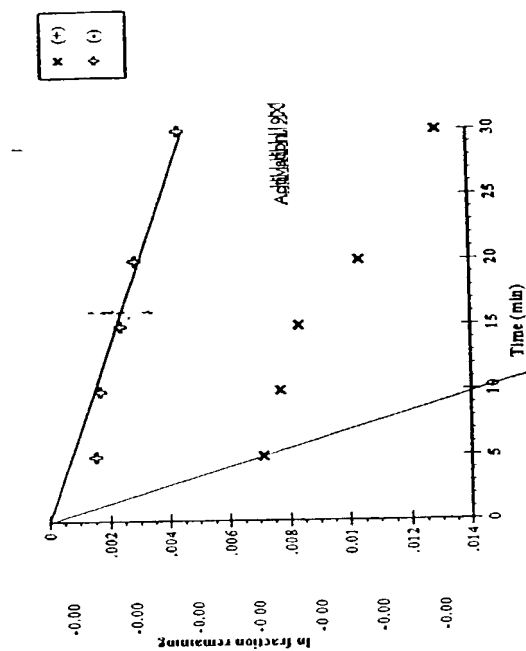


Figure 1 is a 2D chromatogram. The horizontal axis (x-axis) is labeled 'Caffeine' and has tick marks at 5, 10, 15, 20, and 30. The vertical axis (y-axis) is labeled 'Theo' and has tick marks at 5, 10, 15, 20, and 30. The plot area is dark with a grid of horizontal and vertical lines. Two distinct peaks are visible: one at approximately (5, 5) and another at approximately (15, 15). The peak at (5, 5) is labeled 'Caffeine' and the peak at (15, 15) is labeled 'Theo'.

[illegible]

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Figure 3.

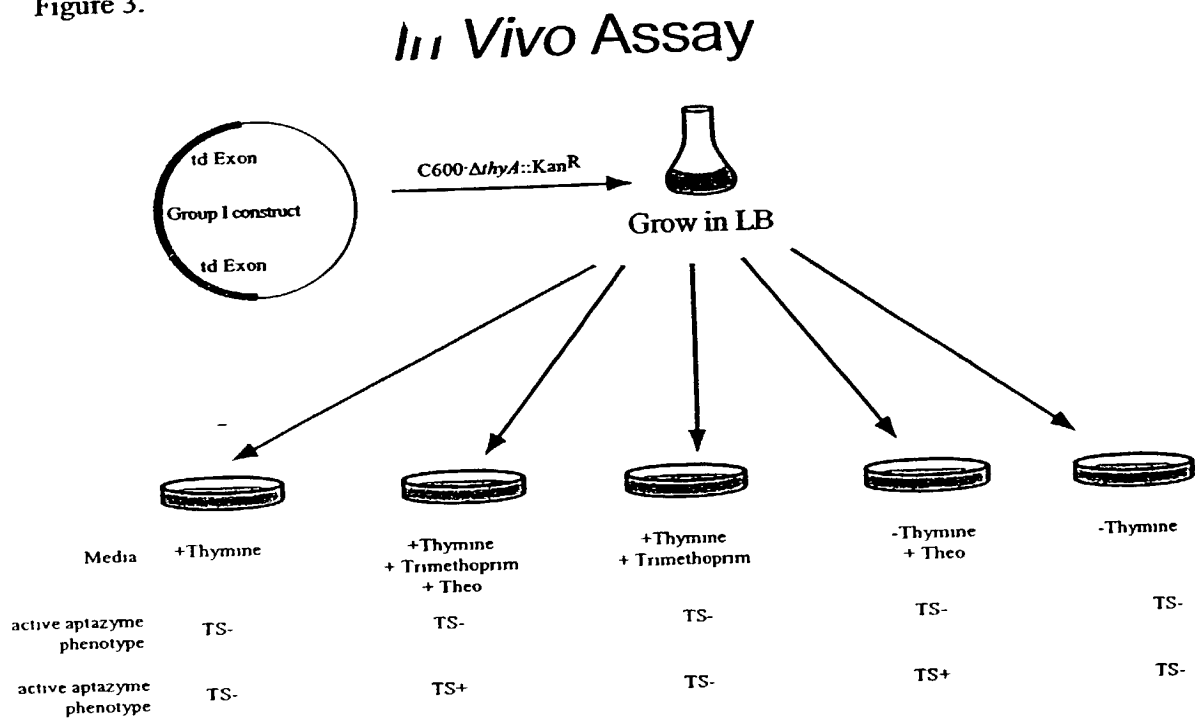
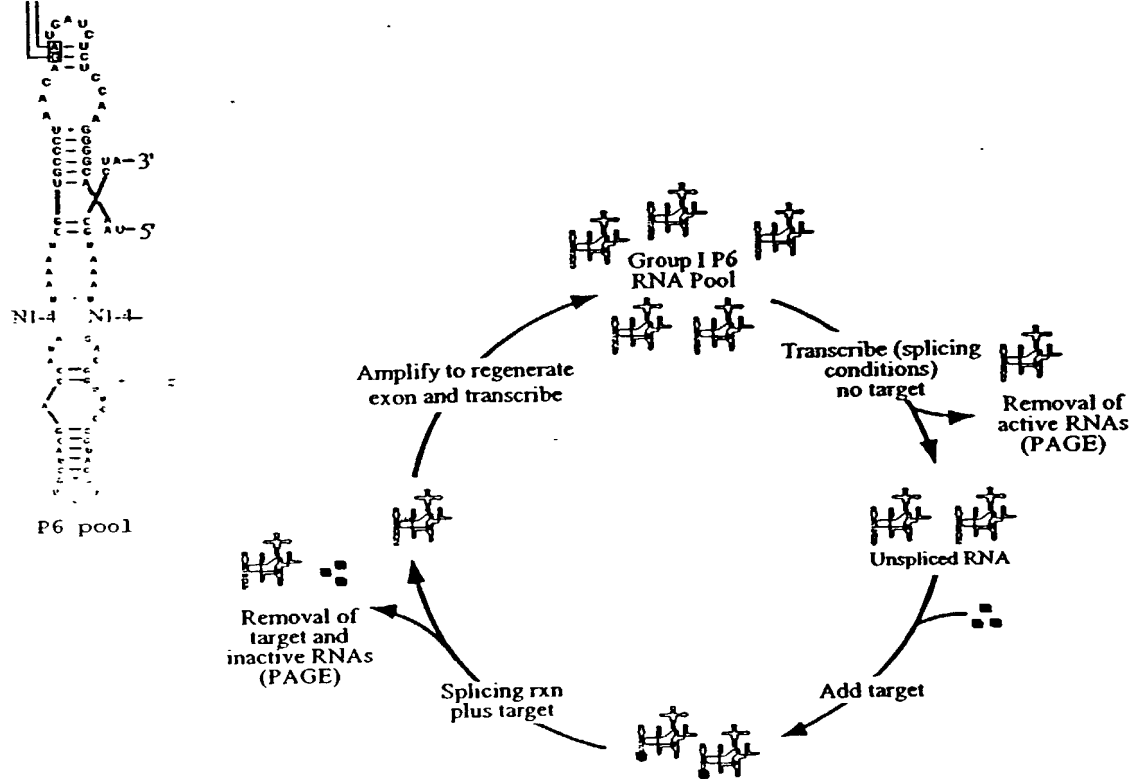


Figure 4.



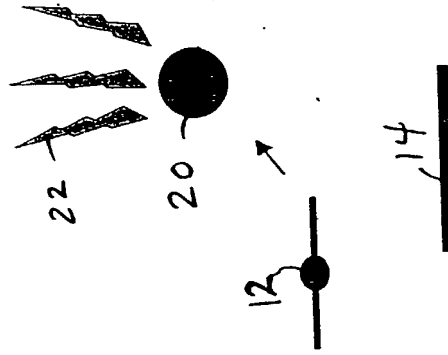
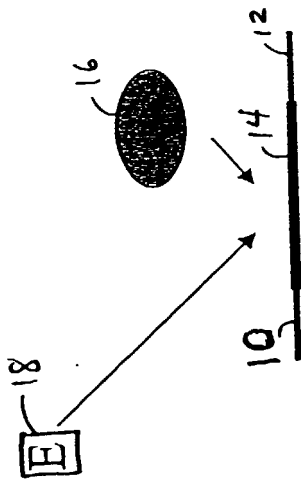


Fig. 5

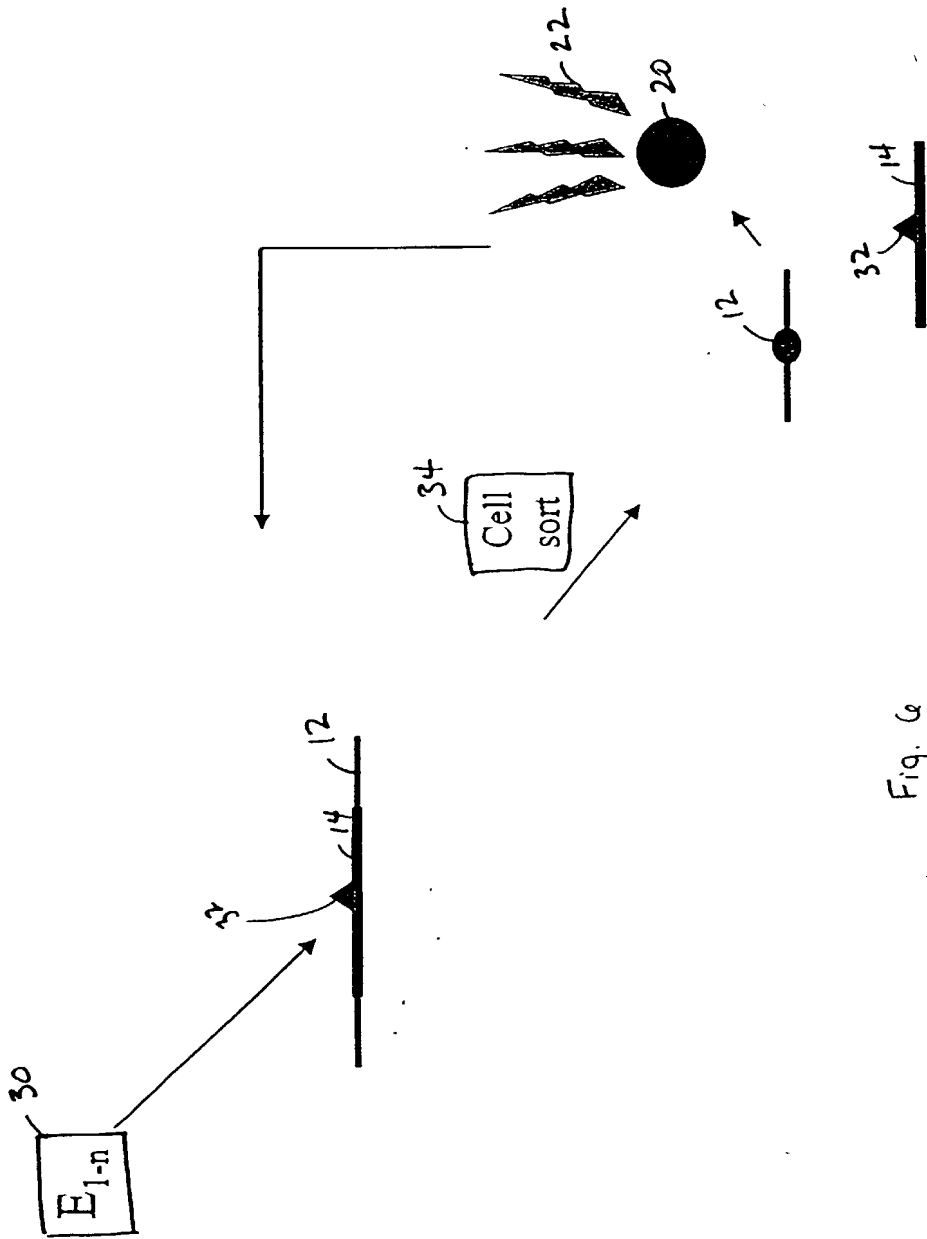
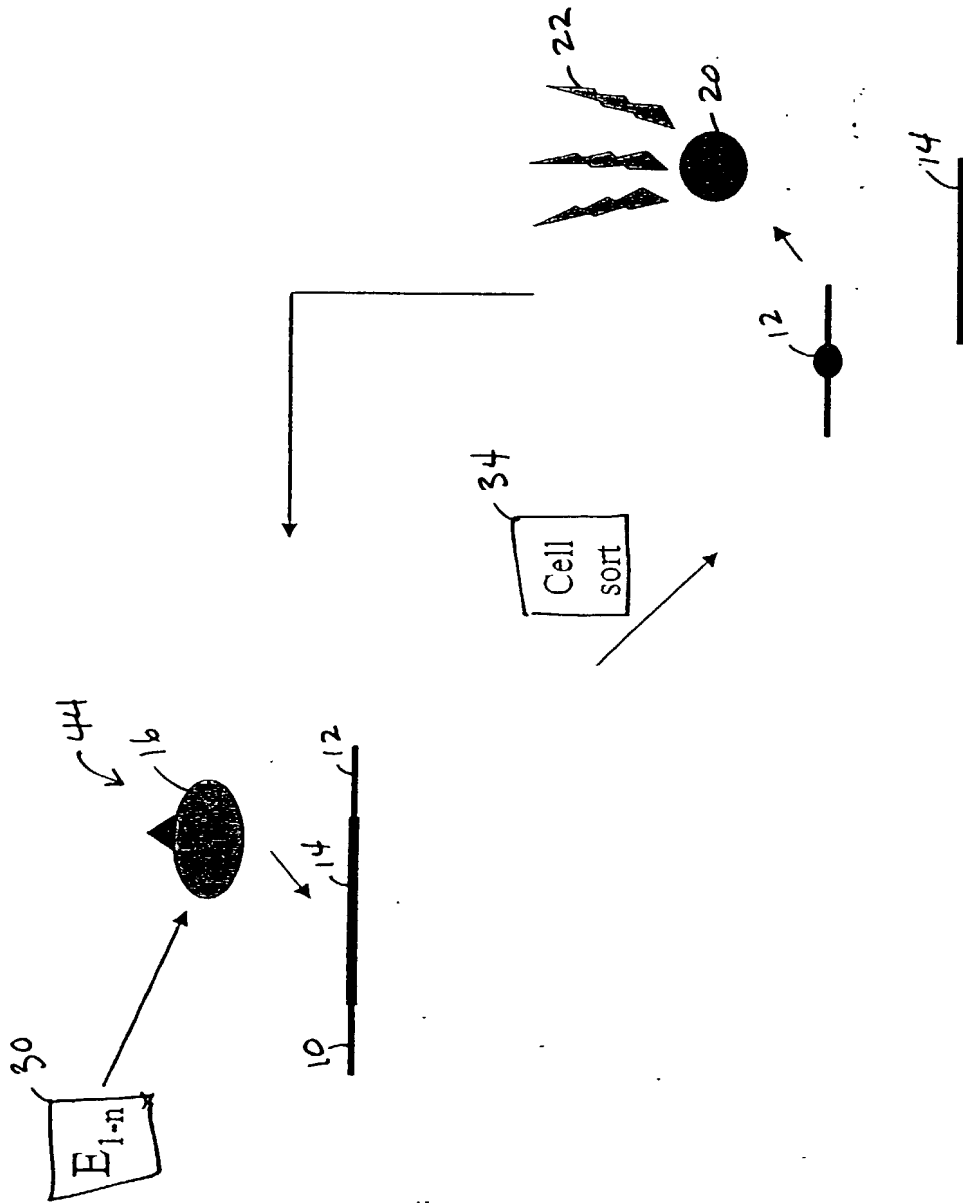


Fig. 6



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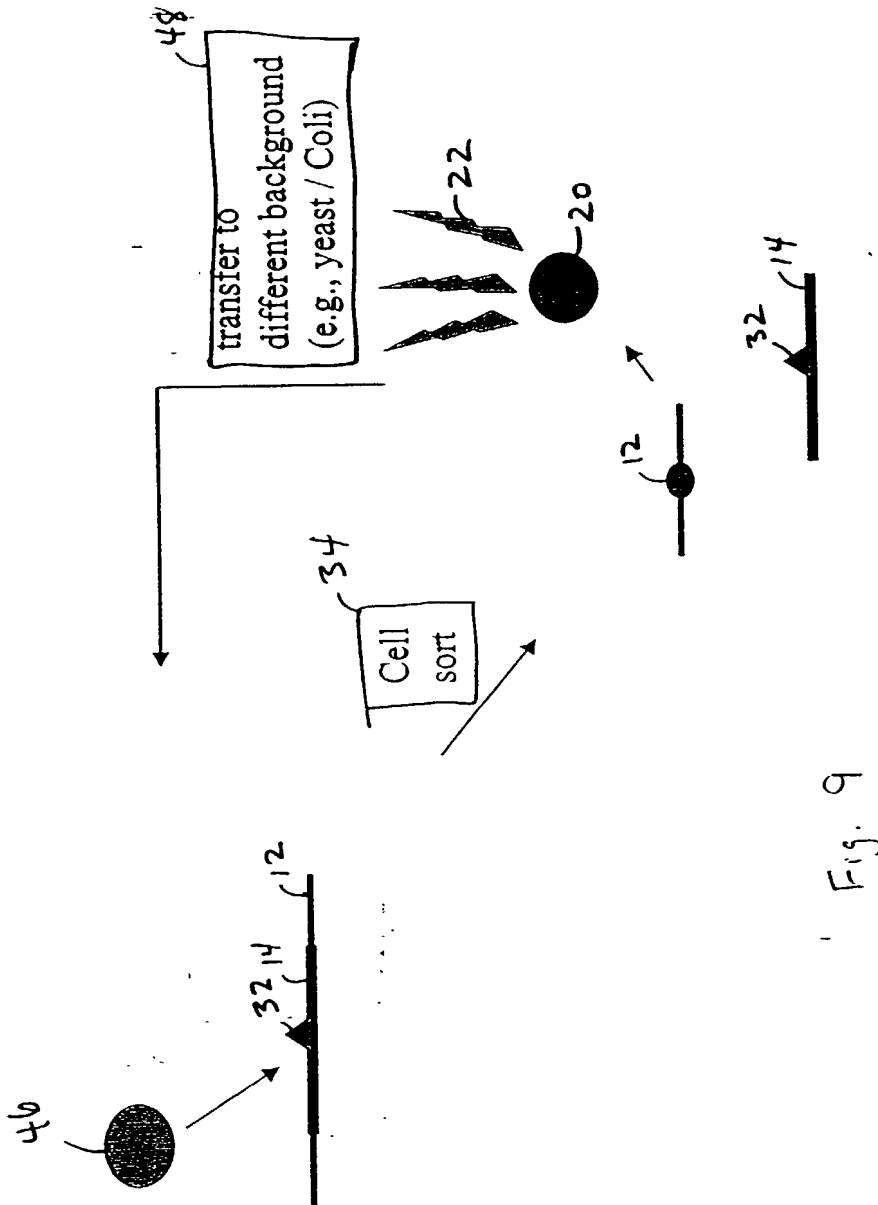


Fig. 9

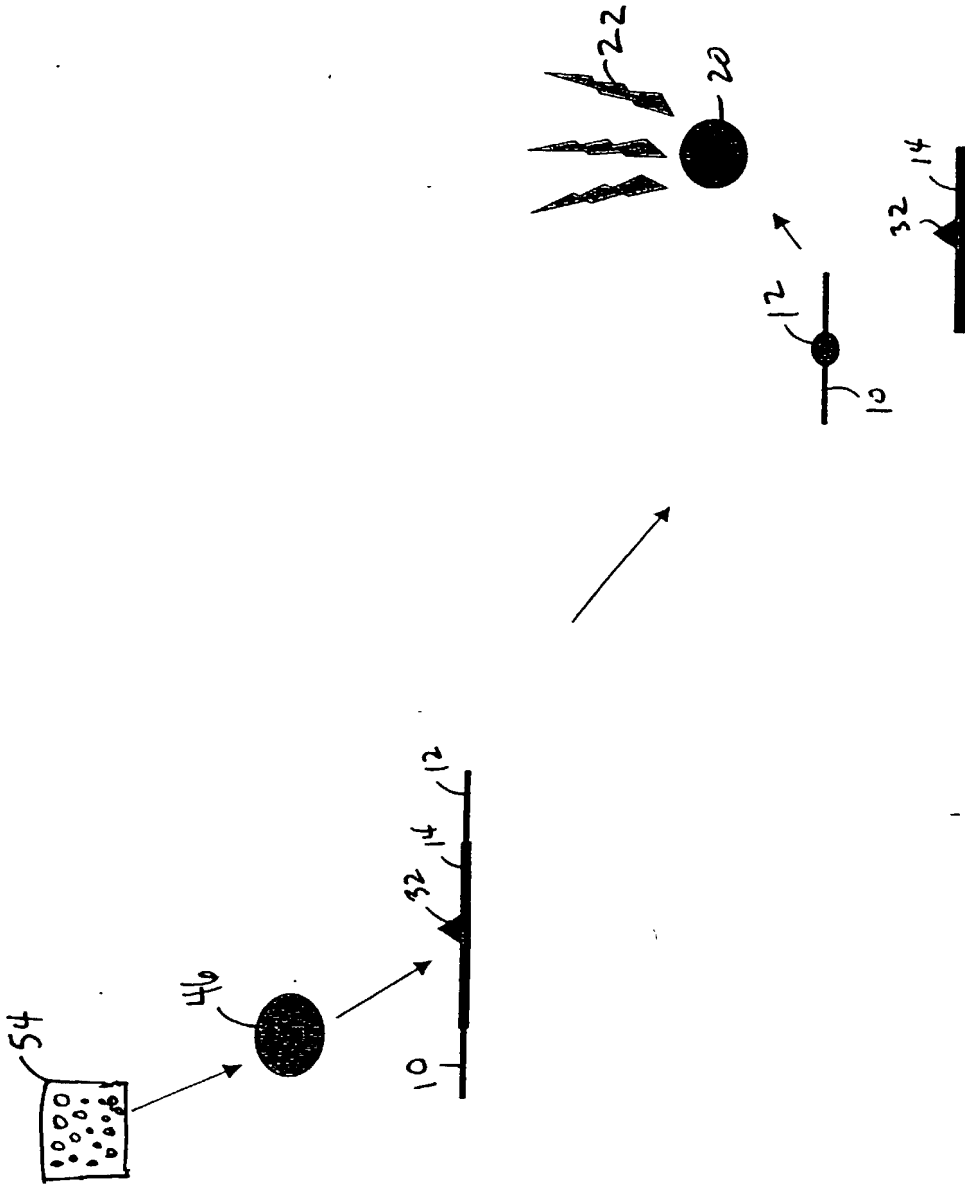


Fig. 11

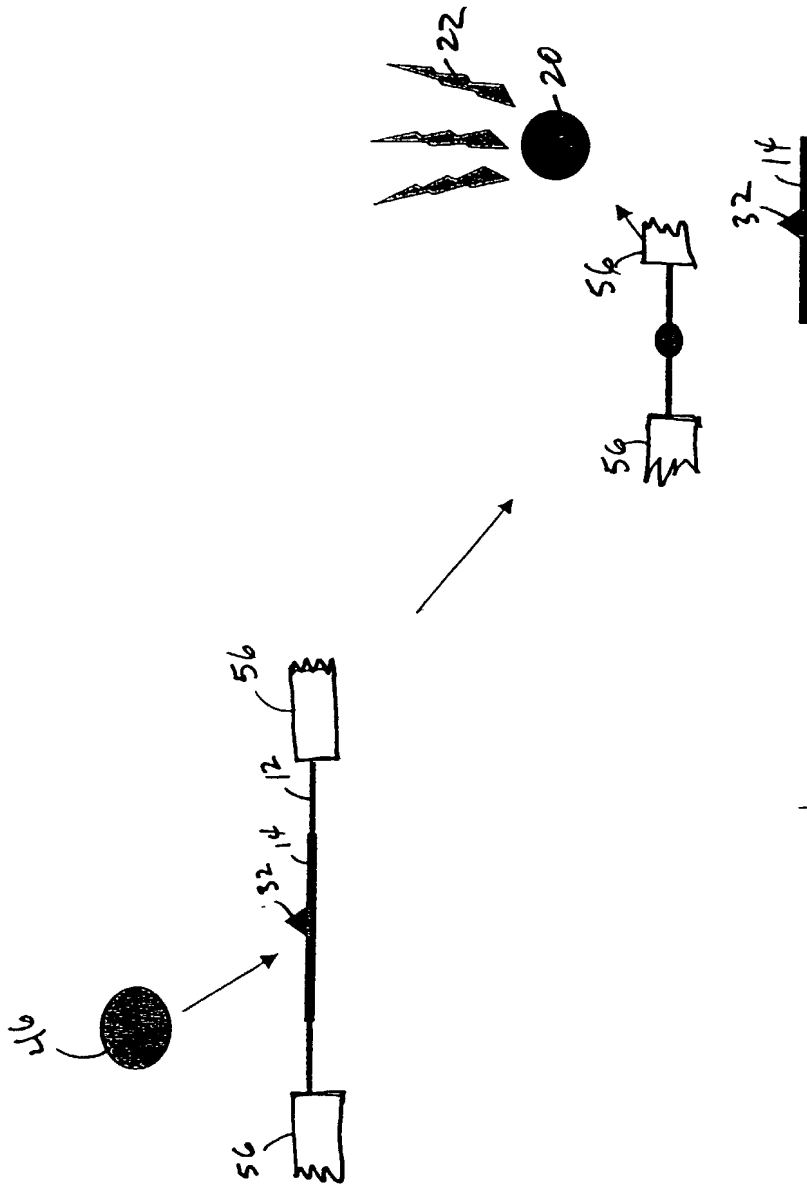


Fig. 12

Direction of movement

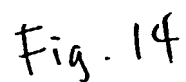


Fig. 15a

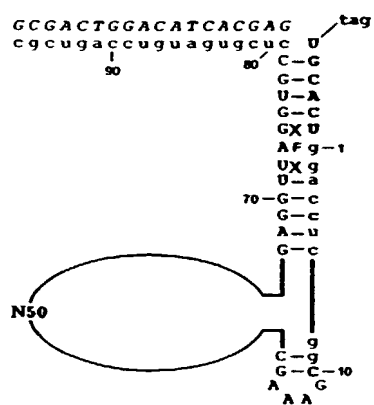


Fig. 15b

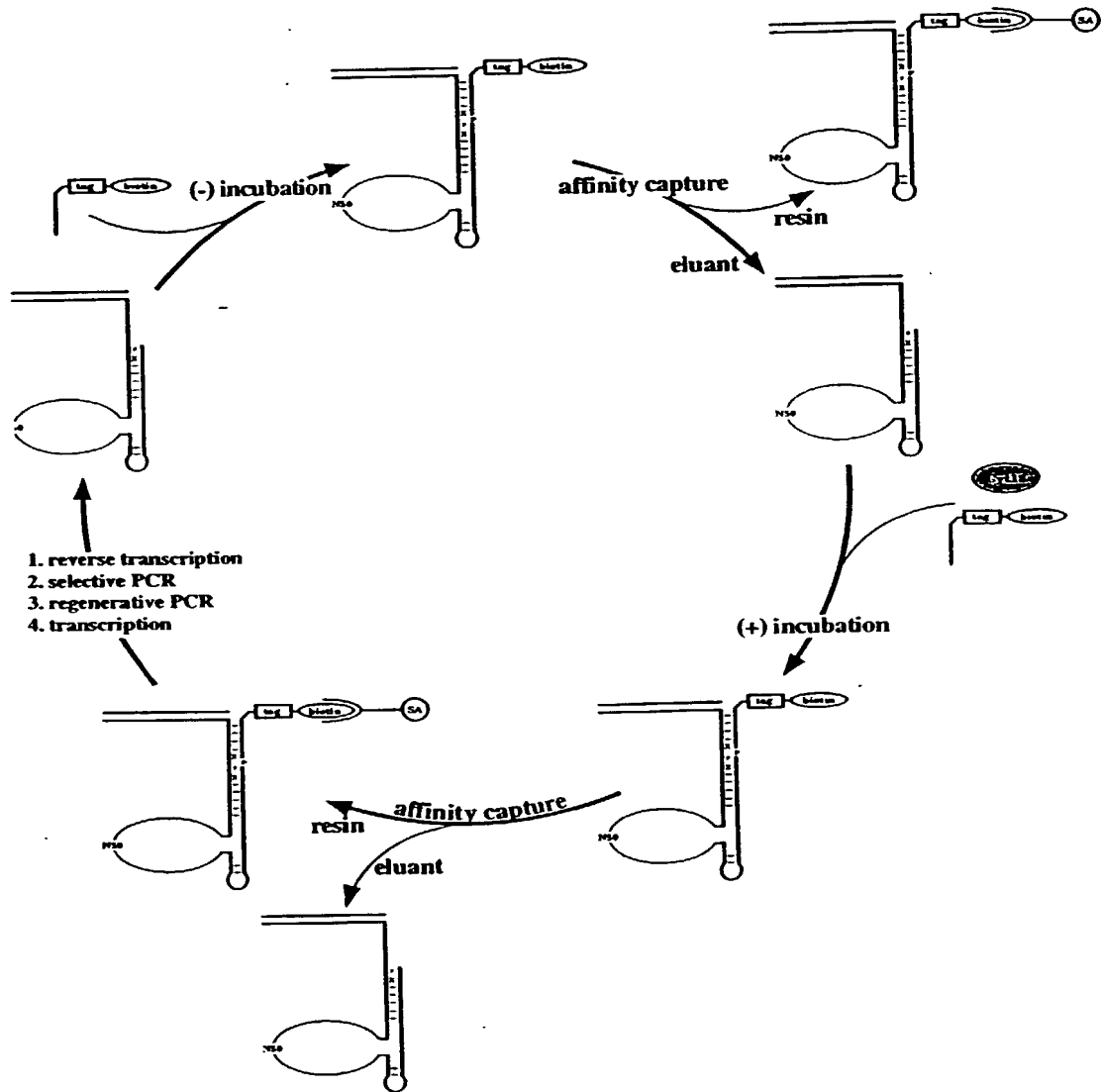


Fig. 15 c

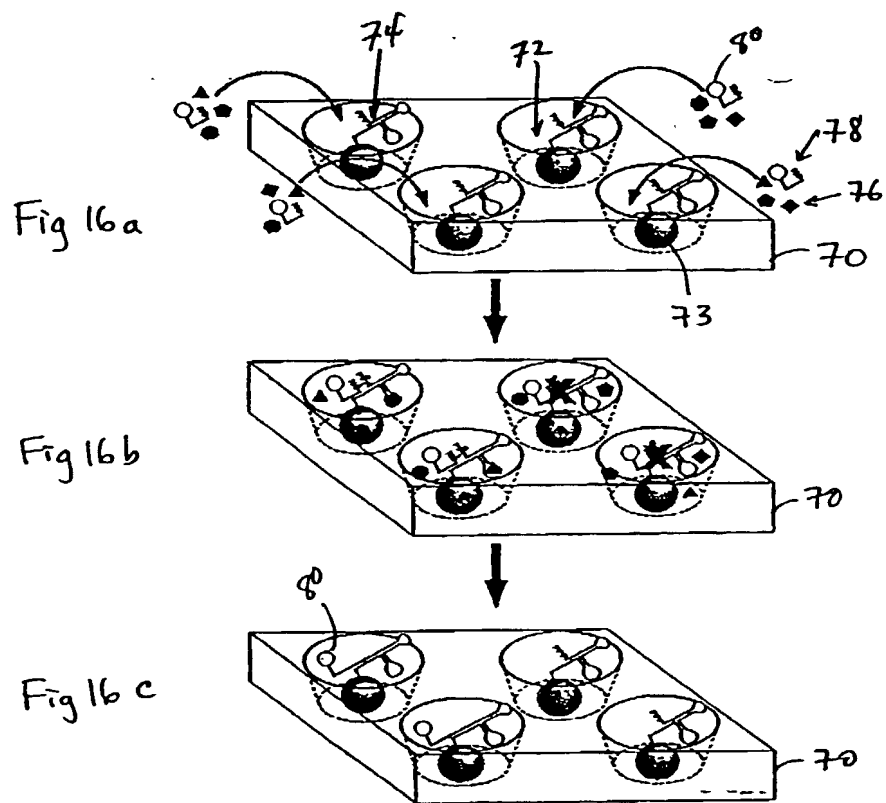


Figure 17

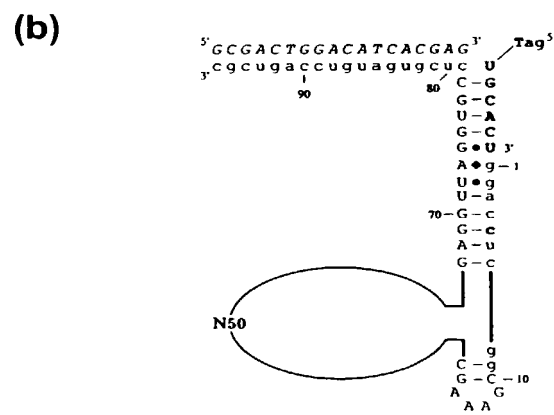
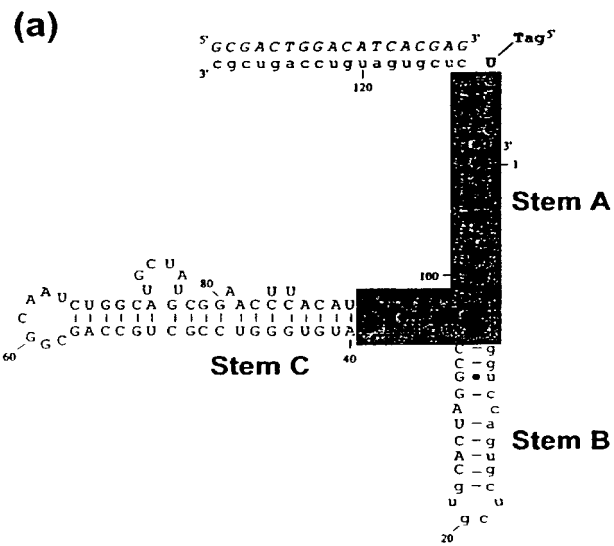




Figure 18

(a)

Round	(-) Incubation		(+) Incubation		Activation
	Substrate	(-) Cyt18	Substrate	(+) Cyt18	
1			2X	14 h	
2	2X	20 h	2X	14 h	
3	2X	20 h	2X	8 h	0.9
4	2X	20 h	2X	1 h	1.0
5	4X	44 h	2X	1 h	26
6	4X	45 h	2X	15 min	1800
7	4X	91 h	2X	5 min	61000
8			1X	30 s	66000
9	4X	20 h	1X	30 s	76000

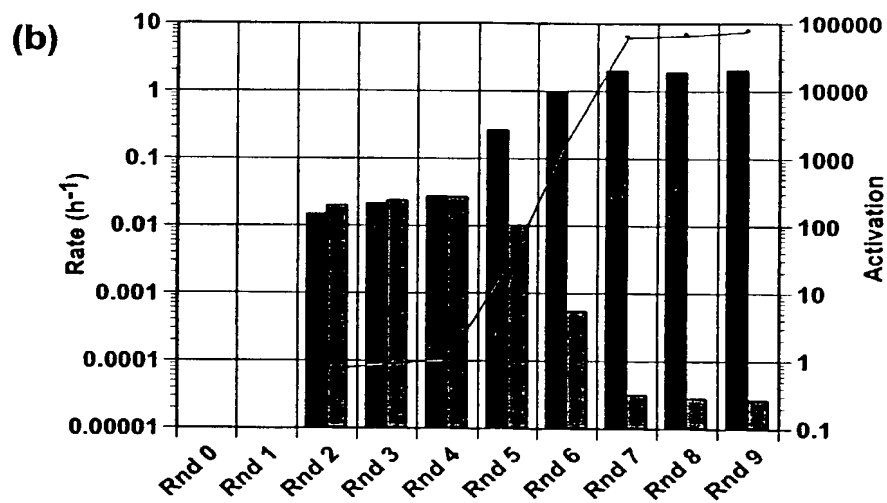


Figure 18

(c)

Round	(-) Incubation		(+) Incubation		Activation
	Substrate	(-) Lys	Substrate	(+) Lys	
1			2X	16 h	
2	2X	22 h	2X	14 h	1.0
3	2X	20 h	2X	8 h	1.0
4	2X	18 h	2X	1 h	1.0
5	4X	44 h	2X	1 h	1.0
6	4X	44 h	2X	15 min	1.7
7	4X	90 h	2X	15 min	5.0
8	4X	93 h	2X	5 min	270
9	4X	92 h	2X	1 min	630
10			1X	30 s	780
11	4X	118 h	1X	30 s	820

(d)

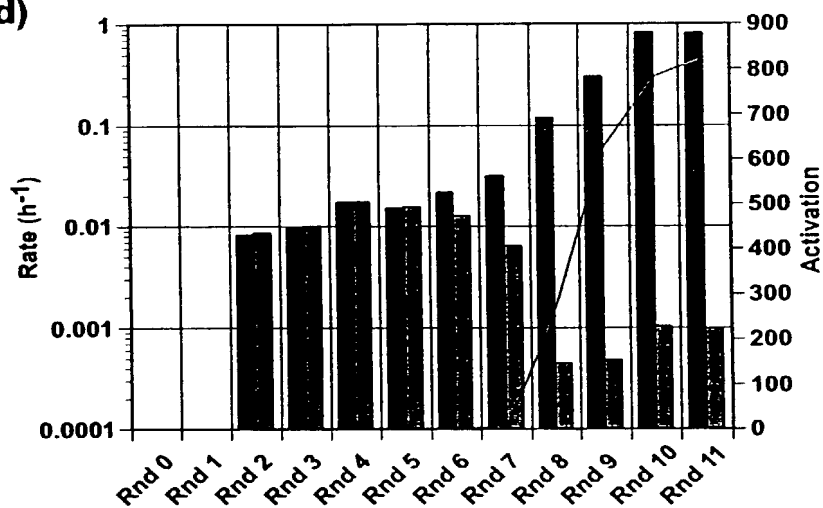
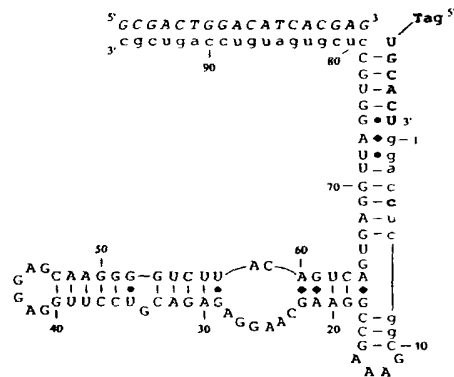


Figure 19

(a)

cyt7-2	(0.61)	CGGAAGCAAGGAGAGACGTCCTTGGAGGAGCAAGGG-----GTCTTACAGTCAGT
cyt7-6	(0.22)	CAGAGCATTAAAG---ACGGGTGACTCTTTAGTTAGGCTCCCCTTAGTCTTAGG
cyt7-1	(0.08)	CAGAGCATGAAGCGGCCACGGGTGCGATGTTGCCCTTG----ETCAGTCTTGGG
cyt9-2	(0.03)	AGGAACCCCCAGATTGTGTCGGGCTGTTATGCGTCGTTTATTGAGATTAC
cyt9-16	(0.03)	CAGTACGTTAATATCCCGGAGCTAGGTGCTTCTTGTGGACAGTTATGGG
cyt9-18	(0.03)	GCACACAGCACTATATTGCTTGGTTCGGAGCGTTTCGTTTATTGAGTTTAC
lys11-2	(0.50)	TAACTCTCATGGCTAAATTGCCATGT-TGCTACAAATGATATGACTAGA
lys11-3	(0.38)	TAACGAAGACTTTGGTGACCGGCTAGTCTTCTATTAATGAGATGACGAGA
lys11-28	(0.08)	TAACTCCCGCACTTAGGAACGGGTGCTGGA-TAAAAATGATATGACGAGA
lys11-6	(0.04)	TTTAAACGAGAGAATTGGCAGTACCGTGCT-GGTTCCGAGATAACGAGA

(b)



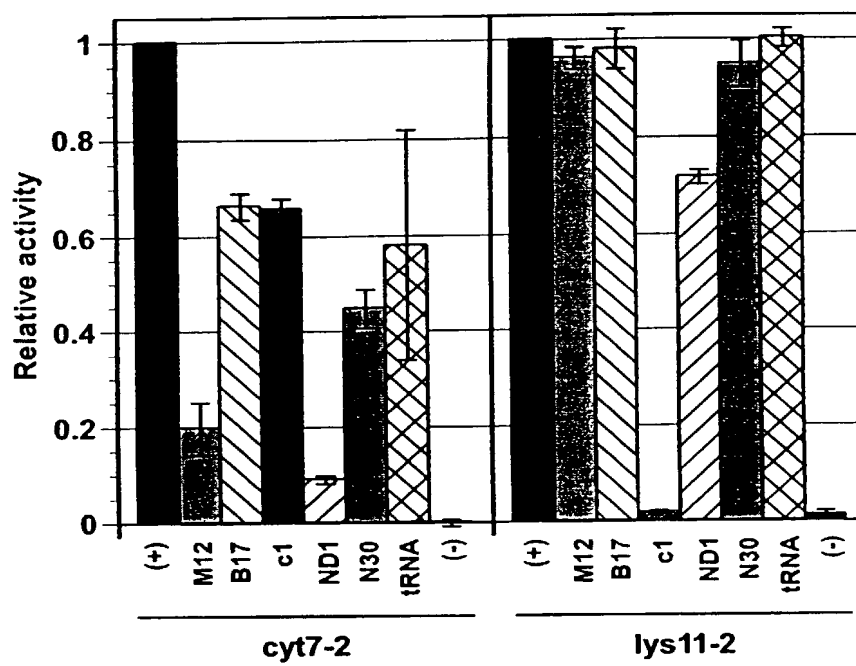


Figure 21

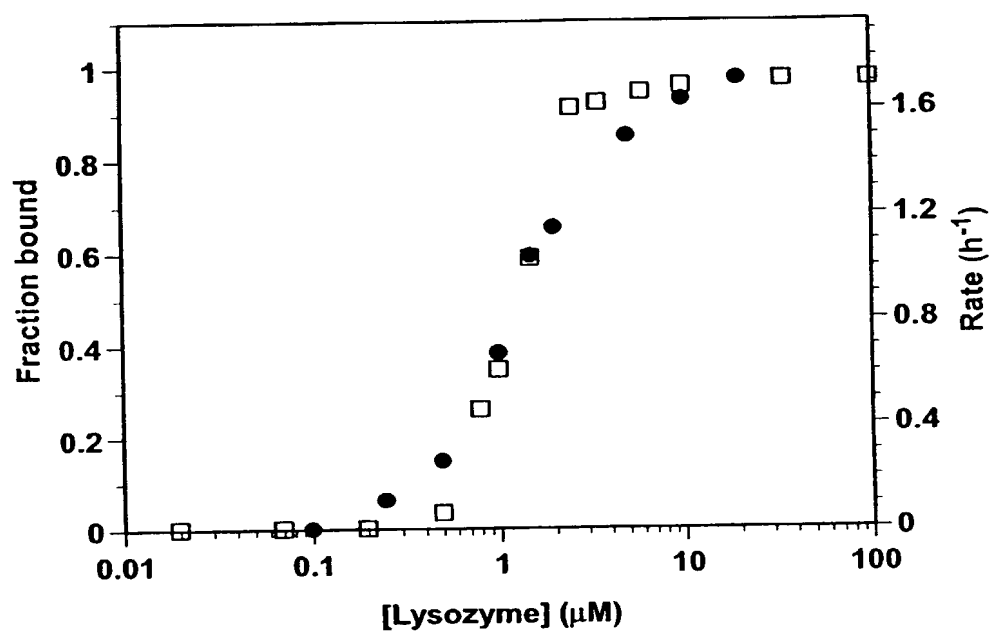


Figure 22

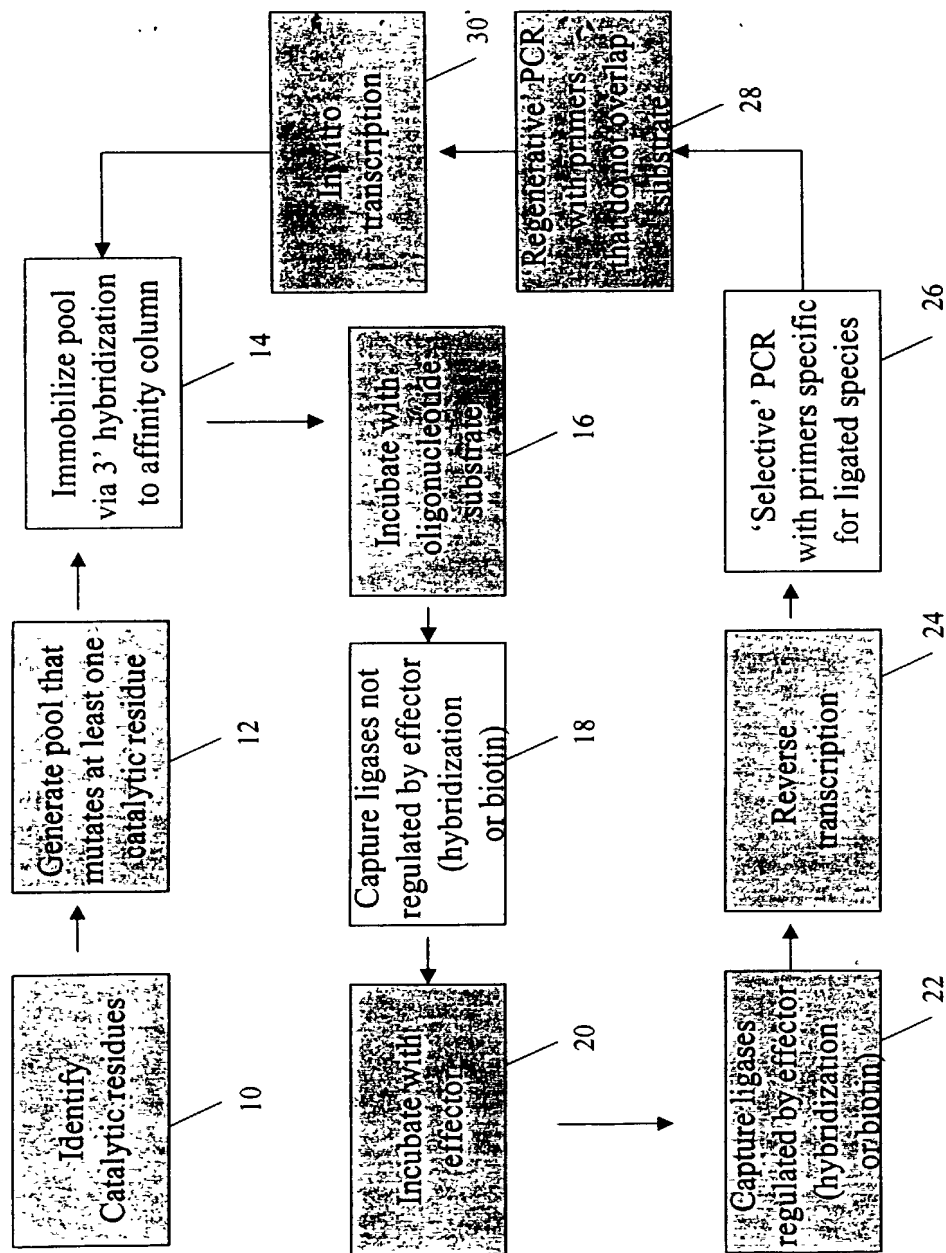
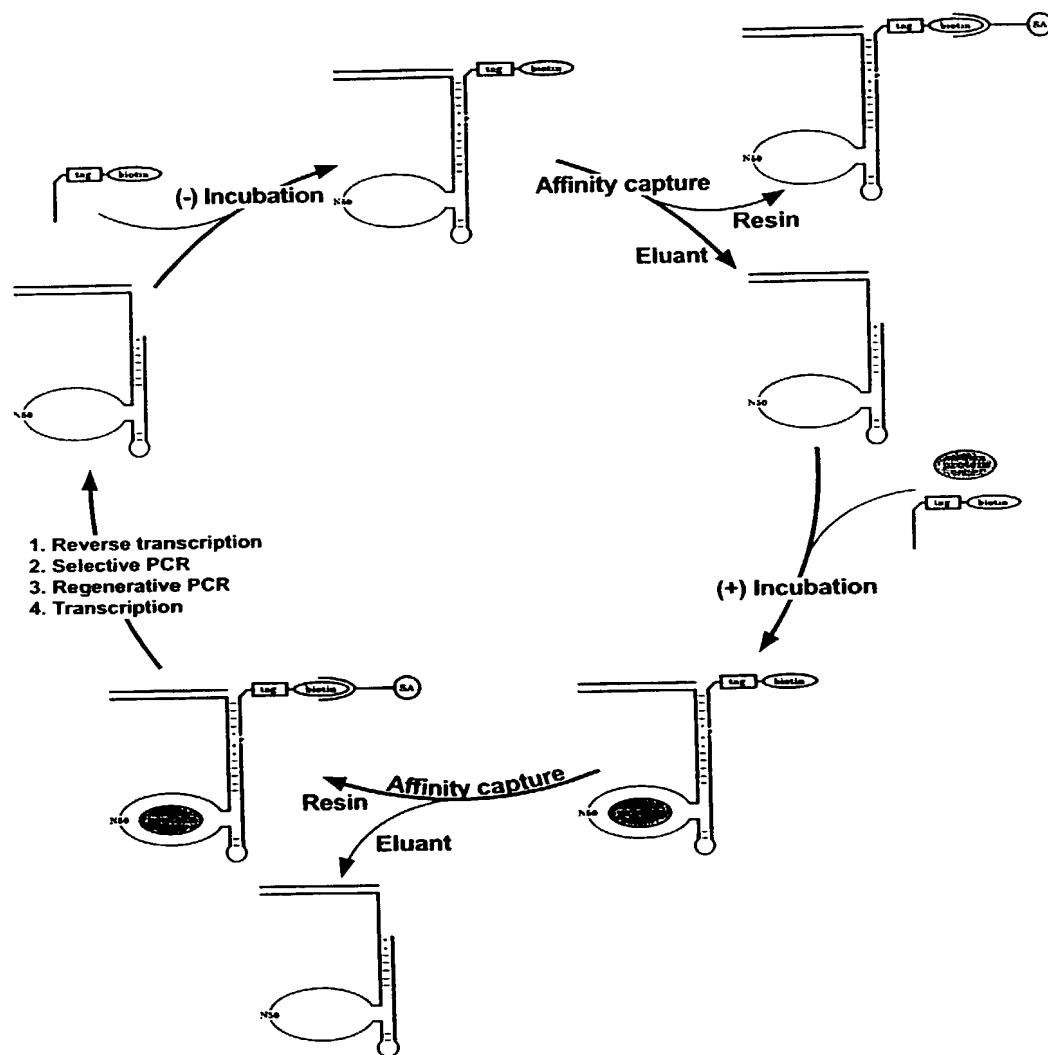


FIGURE 23



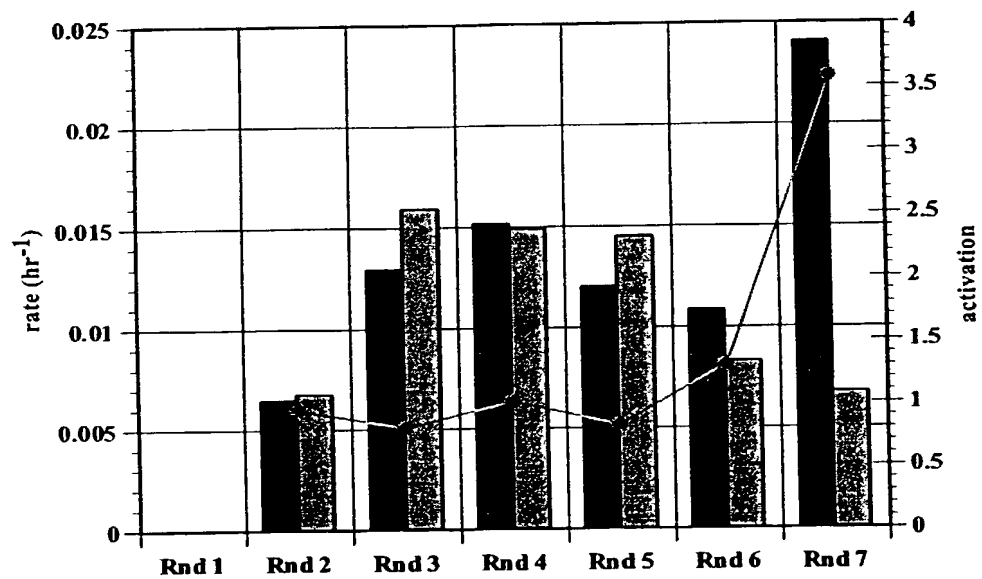
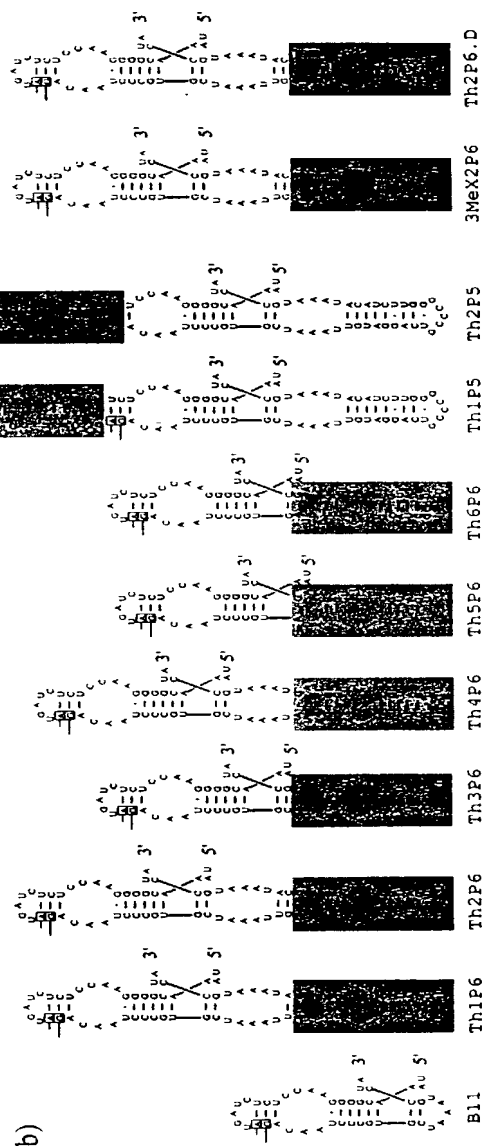
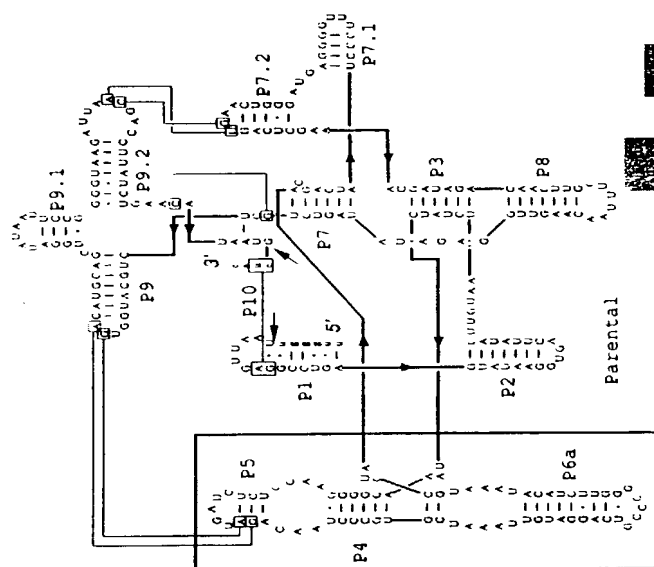


FIGURE 25

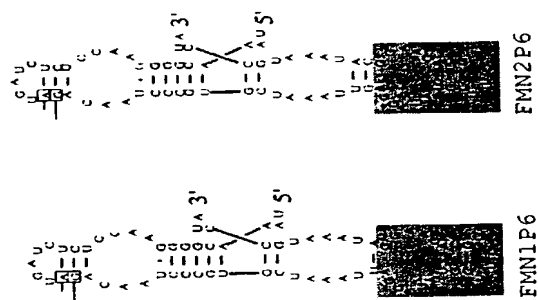


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FIGURE 26



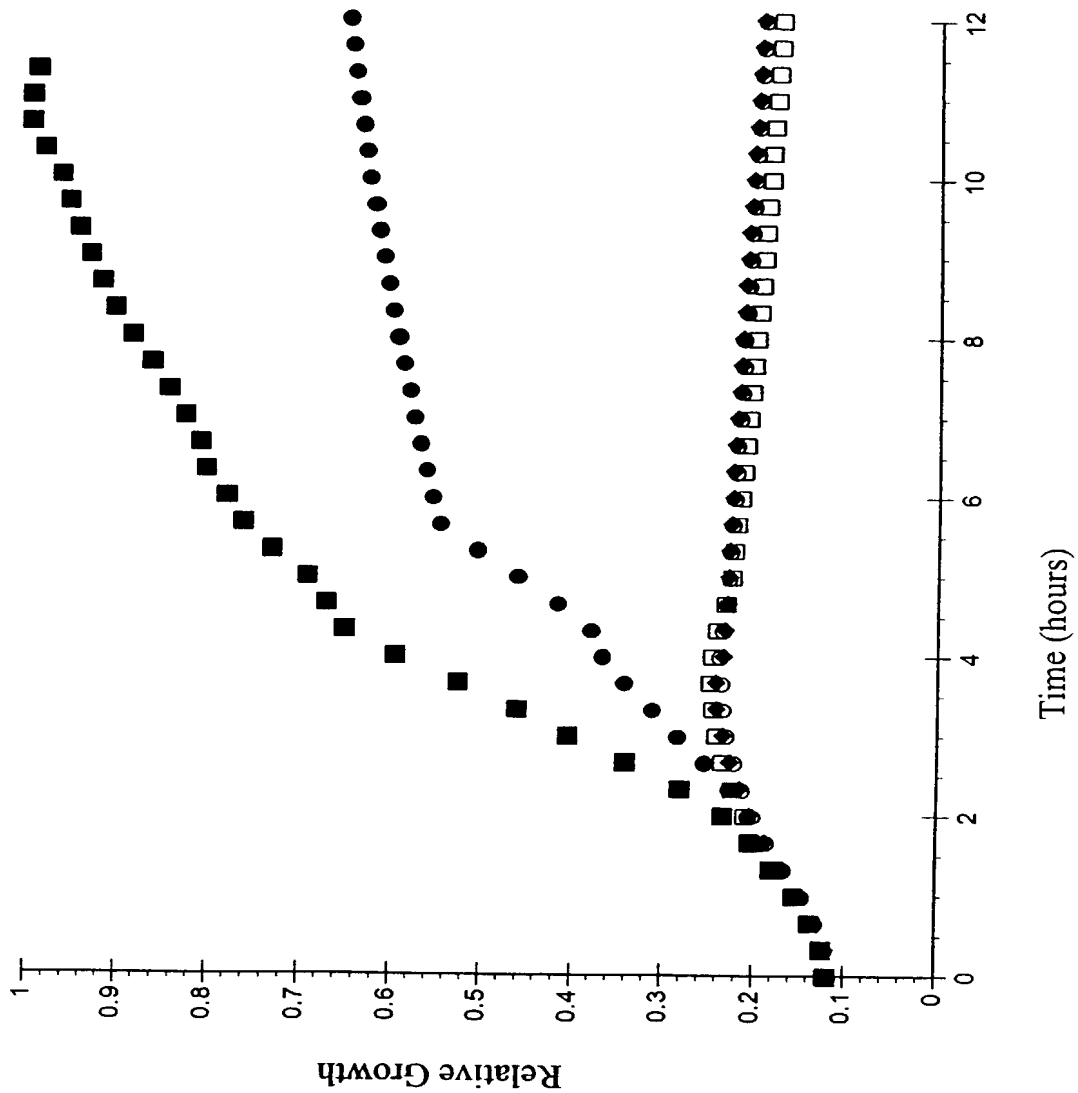


FIGURE 27(a)

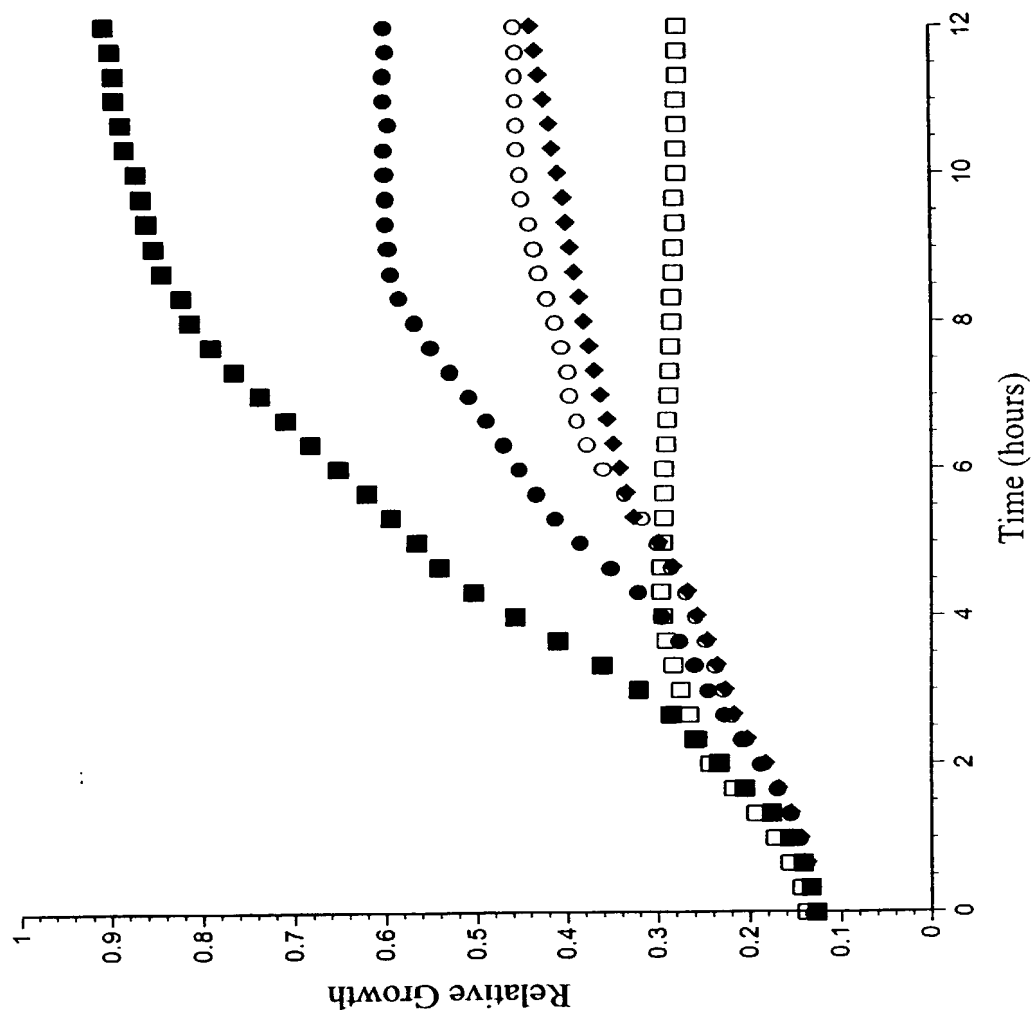


FIGURE 27(b)

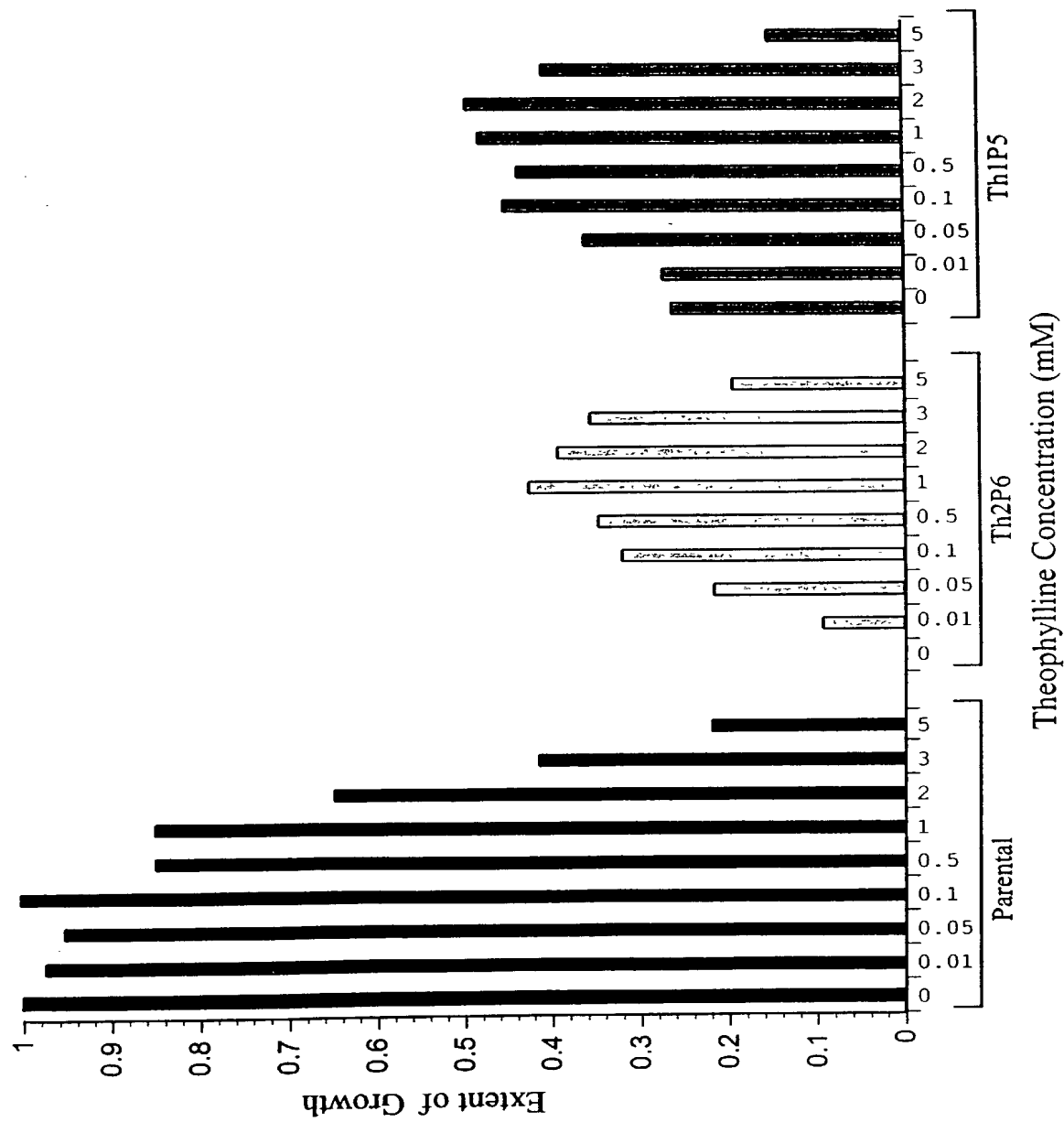


FIGURE 27(c)

FIGURE 28

FIGURE 29

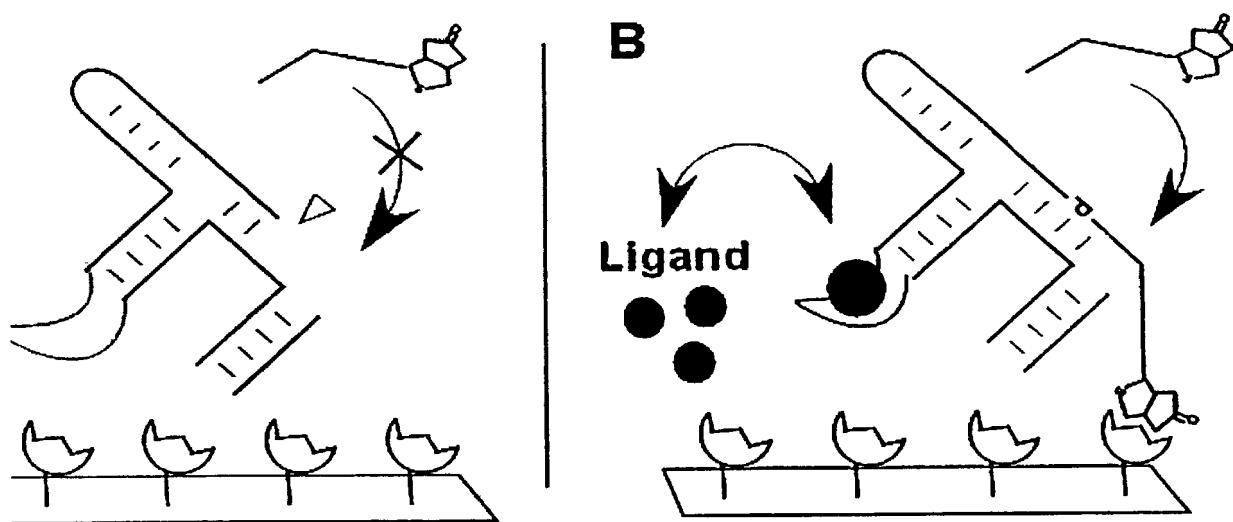


FIGURE 30

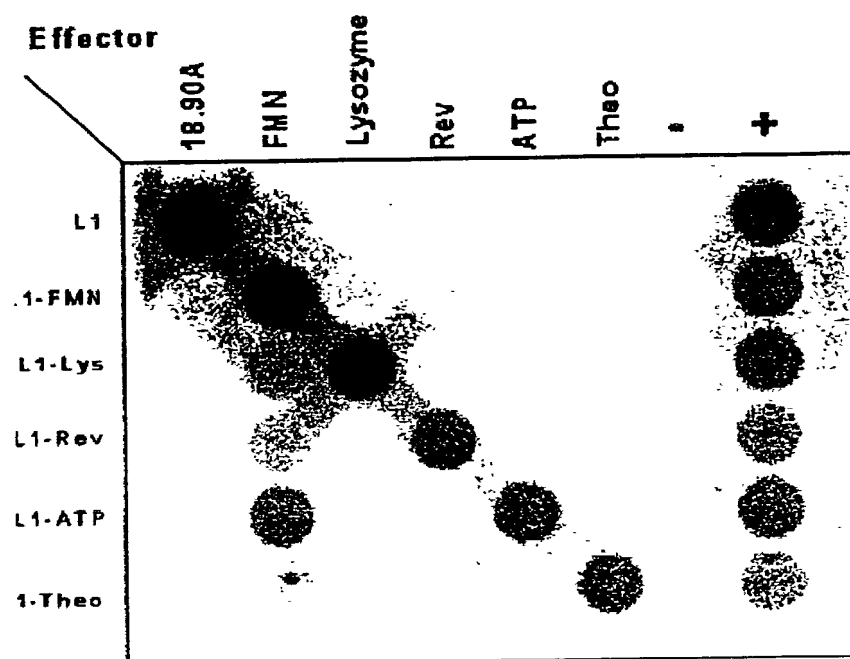
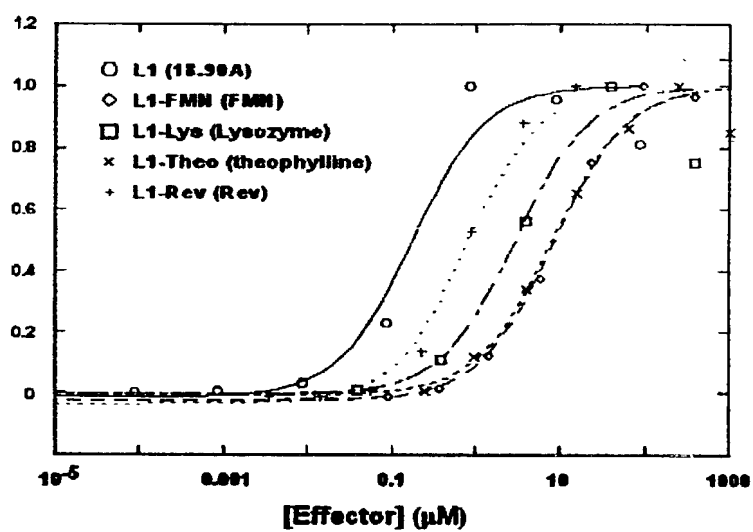


FIGURE 31



<u>Rz</u>	<u>K_d (μM)</u>	<u>% Bound (max)</u>
L1	0.16	16.5
L1-FMN	7.96	14.0
L1-Lys	2.13	22.7
L1-Theo	8.02	3.48
L1-Rev	0.77	19.0